

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2002, 21:30:48 ; Search time 1941.08 Seconds
(without alignments)
2425.696 Million cell updates/sec

Title: US-08-037-230D-18

Perfect score: 225

Sequence: 1 TATTTCTTCTGTGATCTT.....CGGACTGTGCCCTGAGGAG 225

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_hgt:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

ALIGNMENTS

RESULT 1

AR153509

LOCUS

DEFINITION

AR153509

ACCESSION

AR153509.1

VERSION

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE

1 (bases 1 to 225)

AUTHORS

van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.

TITLE

Isolated nucleic acid molecules coding for tumor rejection antigen precursor MAGE-3 and uses thereof

JOURNAL

Patent: US 6235525-A 18 22-MAY-2001;

FEATURES

Location/Qualifiers

source

1..225

/organism="unknown"

BASE COUNT

44 a 65 c 58 g 58 t

Query Match

100.0%

Score 225;

DB 6;

Length 225;

linear PAT 08-AUG-2001

225 bp DNA

Sequence 18 from patent US 6235525.

AR153509

Sequence 18 from patent US 6235525.

AR153509

AR153509.1

GI:15121041

Unknown.

Unclassified.

REFERENCE

1 (bases 1 to 225)

AUTHORS

van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.

TITLE

Isolated nucleic acid molecules coding for tumor rejection antigen precursor MAGE-3 and uses thereof

JOURNAL

Patent: US 6235525-A 18 22-MAY-2001;

FEATURES

Location/Qualifiers

source

1..225

/organism="unknown"

BASE COUNT

44 a 65 c 58 g 58 t

ORIGIN

Query Match 69.8%; Score 157; DB 9; Length 945;
Best Local Similarity 100.0%; Pred. No. 6.3e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATCGAG 63
Db 436 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATCGAG 495

QY 64 CTGATGGAAGTGGACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 123
Db 496 CTGATGGAAGTGGACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 555

QY 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
Db 556 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 592

RESULT 5
LOCUS AR167377 1019 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 13 from patent US 6287569.
ACCESSION AR167377
VERSION AR167377.1 GI:17903153
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1019)
AUTHORS Kippes,T.J. and Wu,Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 13 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..1019
BASE COUNT 224 a 284 c 292 g 219 t
ORIGIN

Query Match 69.8%; Score 157; DB 6; Length 1019;
Best Local Similarity 100.0%; Pred. No. 6.3e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATCGAG 63
Db 501 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATCGAG 560

QY 64 CTGATGGAAGTGGACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 123
Db 561 CTGATGGAAGTGGACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 620

QY 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
Db 621 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 657

RESULT 6
LOCUS HUMMAGEB 1019 bp mRNA linear PRI 07-FEB-1999
DEFINITION Human mRNA for MAGE-6 protein, complete cds.
ACCESSION D32076
VERSION D32076.1 GI:1125015
KEYWORDS MAGE-6 protein; melanoma antigen.
SOURCE Homo sapiens cell-line M73 CDNA to mRNA.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1019)
AUTHORS Imai,Y.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-1994) Yasuhisa Imai, Kurume University School of

Medicine, Immunology; Asahi 67, Kurume, Fukuoka 830, Japan
(Tel:0942-31-7551, Fax:0942-31-7699)
2 (bases 1 to 1019)
AUTHORS Imai,Y., Shichijo,S., Yamada,A., Katayama,T., Yano,H. and Itoh,K.
TITLE Sequence analysis of the MAGE gene family encoding human
tumor-rejection antigens
JOURNAL Gene 160 (2), 287-290 (1995)
MEDLINE 95369706
FEATURES Location/Qualifiers
1..1019
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="M73"
66..1010
/standard_name="melanoma antigen-6"
/note="Nomenclature of MAGE-6 was according to MAGE gene's
27 nucleotide sequences of HLA-A1 binding motif (Traversari
etc., 1992)"
/codon_start=1
/evidence=experimental
/product="MAGE-6 protein"
/protein_id="BAA06842.1"
/db_xref="GI:1125016"
/translation="MPELRSHCKPEEGLEARGEALGLVGAQAPATEGEERASSST
LVEVTIGVPAESPDPSPQSGASSLPTTMYPLWSQSYEDSSNQEESPFPDLE
SEFOAALSRRKVKLVHFLLLKYRAREPVTKAEMLGSVGNWQYFFVIFSKAGDSLO
VFGIELMEVDPIGHVYIFATCLGLSDGLGDNQIMPKTGLIIILAIITAKEGCAPE
EKIWEELSVLEVFEGREDSIFGDPKLLTQYFVOENLYEVROVPGSDPACYEFLWGP
RLIETSYVKVLHHMKISGGPRISYPLLHMAWLEEGEE"
BASE COUNT 224 a 284 c 292 g 219 t
ORIGIN

Query Match 69.8%; Score 157; DB 9; Length 1019;
Best Local Similarity 100.0%; Pred. No. 6.3e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATCGAG 63
Db 501 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATCGAG 560

QY 64 CTGATGGAAGTGGACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 123
Db 561 CTGATGGAAGTGGACCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 620

QY 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
Db 621 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 657

RESULT 7
LOCUS AX019384 1362 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9940188.
ACCESSION AX019384
VERSION AX019384.1 GI:10043354
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1362)
AUTHORS Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
TITLE Tumor-associated antigen derivatives from the mage family, and
nucleic acid sequences encoding them, used for the preparation of
fusion proteins and of compositions for vaccination
Patent: WO 9940188-A 10 12-AUG-1999;
SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
FEATURES Location/Qualifiers
1..1362
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 345 a 348 c 383 g 286 t
ORIGIN /note="Melanoma tissue"

Query Match 69.8%; Score 157; DB 6; Length 1362;

Best Local Similarity 100.0%; Pred. No. 6.3e-81;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAG 63

Db 826 TTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAG 885

QY 64 CTGATGAAGTGGACCCCATCGGCGACGTGTACATCTTTGCCACTCGCTGGGCTCTCC 123

Db 886 CTGATGAAGTGGACCCCATCGGCGACGTGTACATCTTTGCCACTCGCTGGGCTCTCC 945

QY 124 TACATGGCTGCTGGGTGACATCATGATGCCCCA 160

Db 946 TACATGGCTGCTGGGTGACATCATGATGCCCCA 982

RESULT 8

HSU10691 HSI10691 3871 bp DNA linear PRI 23-JUN-1995
LOCUS Human MAGE-6 antigen (MAGE6) gene, complete cds.
DEFINITION
ACCESSION U10691
VERSION U10691.1 GI:533522

SOURCE

human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 3871)

AUTHORS De Plaen, E., Arden, K., Traversari, C., Gaforio, J. J., Szikora, J. P.,

De Smet, C., Brasseur, F., van der Bruggen, P., Lethe, B.,

Lurquin, C., Brasseur, R., Chomez, P., De Backer, O., Cavenne, W. and

Boon, T.

TITLE Structure, chromosomal localization, and expression of 12 genes of

the MAGE family

JOURNAL Immunogenetics 40 (5), 360-369 (1994)

MEDLINE 95012457

REFERENCE 2 (bases 1 to 3871)

AUTHORS De Plaen, E.

TITLE Direct Submission

JOURNAL Submitted (14-JUN-1994) Etienne De Plaen, Ludwig Institute for

Cancer Research, 74 Avenue Hippocrate, Brussels, 1200, Belgium

FEATURES Location/Qualifiers

1..3871

/organism="Homo sapiens"

/isolate="patient M2"

/db_xref="taxon:9606"

/chromosome="X"

/sex="female"

/cell_type="lymphocyte"

/tissue_type="blood"

/dev_stage="adult"

2053..2118

/number=2

2199..>3762

/number=3

2264..3208

/gene="MAGE6"

2264..3208

/gene="MAGE6"

/codon_start=1

/product="MAGE-6 antigen"

/protein_id="AA68875.1"

/db_xref="GI:533523"

/translation="MPLEQRSHCKPEGLRGEALGLVGAQAPATEQEAASSST

LVEVTGLVEPAESPPDPOGASSLPTTMYPLWSQVSDSSNOEGPSTFPDLE

SEFQAALSRVAKLVHLLKRYAREPVTAKMLGVSVGNQVFFPVIFSKDSLQL

VFGIELMEVDPIGHVYIFATCLGLSLDGLDQNPMTGFLIIILAIKESGDAPE

EXINBELSVLEVFEGREDSIFGDPKLLTOYFQBNYLEYRQVPGSDPACYEFLWGP
ALIIETSYKVLHMHMKISGGPRISPLLHWEALREGE"

BASE COUNT 865 a 1050 c 1117 g 839 t
ORIGIN

Query Match 69.8%; Score 157; DB 9; Length 3871;

Best Local Similarity 100.0%; Pred. No. 6.6e-81;

Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAG 63

Db 2699 TTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAG 2758

QY 64 CTGATGAAGTGGACCCCATCGGCGACGTGTACATCTTTGCCACTCGCTGGGCTCTCC 123

Db 2759 CTGATGAAGTGGACCCCATCGGCGACGTGTACATCTTTGCCACTCGCTGGGCTCTCC 2818

QY 124 TACATGGCTGCTGGGTGACATCATGATGCCCCA 160

Db 2819 TACATGGCTGCTGGGTGACATCATGATGCCCCA 2855

RESULT 9

AF002997 AF002997 245077 bp DNA linear PRI 13-APR-2001
LOCUS Homo sapiens chromosome X map Xq28, complete sequence.
DEFINITION
ACCESSION AF002997
VERSION AF002997.2 GI:13621226

KEYWORDS HTG; HTGS_ACTIVEFIN.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 9444 to 72299)

AUTHORS Gloeckner, G., Rosenthal, A., Drescher, B., Schattevoy, R., Poustka, A.,

and Kioschis, P.

TITLE Genomic sequence in Xq28

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 245077)

AUTHORS Galocz, P., Schilhabel, M., Rosenthal, A. and Platzter, M.

TITLE Chromosome X genomic sequence

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 245077)

AUTHORS Gloeckner, G., Rosenthal, A., Drescher, B. and Schattevoy, R.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-1997) Genome Analysis, Institute of Molecular

Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

REFERENCE 4 (bases 1 to 245077)

AUTHORS Platzter, M.

TITLE Direct Submission

JOURNAL Submitted (13-APR-2001) Genome Analysis, Institute of Molecular

Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

COMMENT On Apr 13, 2001 this sequence version replaced gi:4409798.

FEATURES Location/Qualifiers

1..245077

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="X"

/map="Xq28"

1..211945

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="RP1-14D6"

/clone_lib="RPCI human PAC library 1"

9444..45606

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="LM0411, cosmid"

20074..226999

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CTD-2530F8"

```
/clone_lib="CalTech human BAC library D"
33939..72299
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="LO0630, cosmid"
42555..245077
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CTD-2507L14"
/clone_lib="CalTech human BAC library D"
70149 a 53336 c 52595 g 68996 t 1 others
BASE COUNT 70149 a 53336 c 52595 g 68996 t 1 others
ORIGIN

Query Match 69.8%; Score 157; DB 9; Length 245077;
Best Local Similarity 100.0%; Pred. No. 7.6e-81;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGGCAGCTGGTCTTTGGCATCGAG 63
Db 164123 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGGCAGCTGGTCTTTGGCATCGAG 164182

Qy 64 CTGATGAAGTGAGCCCGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 123
Db 164183 CTGATGAAGTGAGCCCGCCAGCTGTACATCTTTGCCACCTGCCCTGGGCTCTCC 164242

Qy 124 TACGATGGCTGTGGGTGACATCAGATCATGCCCA 160
Db 164243 TACGATGGCTGTGGGTGACATCAGATCATGCCCA 164279

RESULT 10
AX019380
LOCUS AX019380 1212 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 6 from Patent WO9940188.
ACCESSION AX019380
VERSION AX019380.1 GI:10043352
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1212)
AUTHORS Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
TITLE Tumor-associated antigen derivatives from the mage family, and
nucleic acid sequences encoding them, used for the preparation of
fusion proteins and of compositions for vaccination
JOURNAL Patent: WO 9940188-A 6 12-AUG-1999;
SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
FEATURES
source
LOCATION/Qualifiers
1..1212
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Melanoma tissue"
BASE COUNT 289 a 319 c 344 g 260 t
ORIGIN

Query Match 32.9%; Score 74; DB 6; Length 1212;
Best Local Similarity 99.2%; Pred. No. 4.1e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 36 TTCCTTGACGTGGTCTTTGGCATCGAGCTGATGAAGTGACCCCATCGCCACGTGTA 95
Db 708 TTCCTTGACGTGGTCTTTGGCATCGAGCTGATGAAGTGACCCCATCGCCACGTGTA 767

Qy 96 CATCTTTGCCACCTGCCCTCTCTCTAGATGGCTGCTGGTGACAAATCAGATCAT 155
Db 768 CATCTTTGCCACCTGCCCTCTCTCTAGATGGCTGCTGGTGACAAATCAGATCAT 827

Qy 156 GCCCA 160
|||||

Query Match 32.9%; Score 74; DB 6; Length 1353;
Best Local Similarity 99.2%; Pred. No. 4.1e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 36 TTCCTTGACGTGGTCTTTGGCATCGAGCTGATGAAGTGACCCCATCGCCACGTGTA 95
Db 849 TTCCTTGACGTGGTCTTTGGCATCGAGCTGATGAAGTGACCCCATCGCCACGTGTA 908

Qy 96 CATCTTTGCCACCTGCCCTCTCTCTAGATGGCTGCTGGTGACAAATCAGATCAT 155
Db 909 CATCTTTGCCACCTGCCCTCTCTCTAGATGGCTGCTGGTGACAAATCAGATCAT 968

Qy 156 GCCCA 160
|||||

RESULT 12
AX343855
LOCUS AX343855 1569 bp DNA linear PAT 01-FEB-2002
DEFINITION Sequence 1 from Patent WO0200892.
ACCESSION AX343855
VERSION AX343855.1 GI:18491925
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (sites)
AUTHORS cabezon Silva,T.E. and Delisse,A.M.
TITLE Triple fusion proteins comprising ubiquitin fused between
thioredoxin and a polypeptide of interest
JOURNAL Patent: WO 0200892-A 1 03-JAN-2002;
SMITHKLINE Beecham Biologics SA (BE)
FEATURES
source
LOCATION/Qualifiers
1..1569
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Chimaeric (E. coli - human)"
BASE COUNT 391 a 400 c 433 g 345 t
ORIGIN
```

```
Query Match      32.9%; Score 74; DB 6; Length 1569;
Best Local Similarity 99.2%; Pred. No. 4.2e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGTCCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
|||||
Db 1065 TTCCTTGCAGCTGTCCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 1124
|||||
QY 96 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 1125 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 1184
|||||
QY 156 GCCCA 160
|||||
Db 1185 GCCCA 1189

RESULT 13
LOCUS      AR153502      1640 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6235525.
ACCESSION  AR153502
VERSION     AR153502.1 GI:15121034
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1640)
AUTHORS    van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.
TITLE      Isolated nucleic acid molecules coding for tumor rejection antigen
JOURNAL    precursor MAGE-3 and uses thereof
FEATURES   Location/Qualifiers
            source          1..1640
            BASE COUNT      380 a 402 c 457 g 401 t
            ORIGIN

Query Match      32.9%; Score 74; DB 6; Length 1640;
Best Local Similarity 99.2%; Pred. No. 4.2e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGTCCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
|||||
Db 1065 TTCCTTGCAGCTGTCCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 1124
|||||
QY 96 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 1125 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 1184
|||||
QY 156 GCCCA 160
|||||
Db 1185 GCCCA 1189

RESULT 13
LOCUS      AR153502      1640 bp      DNA      linear      PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6235525.
ACCESSION  AR153502
VERSION     AR153502.1 GI:15121034
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1640)
AUTHORS    van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.
TITLE      Isolated nucleic acid molecules coding for tumor rejection antigen
JOURNAL    precursor MAGE-3 and uses thereof
FEATURES   Location/Qualifiers
            source          1..1640
            BASE COUNT      380 a 402 c 457 g 401 t
            ORIGIN

Query Match      32.9%; Score 74; DB 6; Length 1640;
Best Local Similarity 99.2%; Pred. No. 4.2e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGTCCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
|||||
Db 639 TTCCTTGCAGCTGTCCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 698
|||||
QY 96 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 699 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 758
|||||
QY 156 GCCCA 160
|||||
Db 759 GCCCA 763

RESULT 14
LOCUS      I36926      1640 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION Sequence 11 from patent US 5612201.
ACCESSION  I36926
VERSION     I36926.1 GI:2084886
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 1640)
AUTHORS    De Plaen,E., Boon-Falleur,T., Lethe,B., Szikora,J.-P., De Smet,C.
            and Chomez,P.
TITLE      Isolated nucleic acid molecules useful in determining expression of
            a tumor rejection antigen precursor
JOURNAL    Patent: US 5612201-A 11 18-MAR-1997;
FEATURES   Location/Qualifiers
            source          1..1640
            BASE COUNT      380 a 402 c 457 g 401 t
            ORIGIN

Query Match      32.9%; Score 74; DB 6; Length 1640;
Best Local Similarity 99.2%; Pred. No. 4.2e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCAGCTGTCCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
|||||
Db 639 TTCCTTGCAGCTGTCCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 698
|||||
QY 96 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 699 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 758
|||||
QY 156 GCCCA 160
|||||
Db 759 GCCCA 763

RESULT 15
LOCUS      BC011744      1663 bp      mRNA      linear      PRI 02-AUG-2001
DEFINITION Homo sapiens, Similar to melanoma antigen, family A, 3, clone
ACCESSION  MGC:19667 IMAGE:3345801, mRNA, complete cds.
VERSION     BC011744
KEYWORDS    MGC.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            REFERENCE       1 (bases 1 to 1663)
            AUTHORS        Strausberg,R.
            TITLE          Direct Submission
            JOURNAL        Submitted (30-JUL-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            REMARK         NIH-MGC Project URL: http://mgc.nci.nih.gov
            COMMENT         Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DMP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site:      http://www.nisc.nih.gov/
            Contact:      nisc_mgc@nhgri.nih.gov
            Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
            Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
            Tlionson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
            Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAL Plate: 27 Row: b Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
            Location/Qualifiers
            source          1..1663
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="MGC:19667 IMAGE:3345801"
            /tissue_type="Skin, melanotic melanoma."
```

```

/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
/notes="Vector: pOTB7"
145..1089
/codon_start=1
/product="Similar to melanoma antigen, family A, 3"
/protein_id="AAH11744.1"
/db_xref="GI:15079898"
/translation="MPLEORSQHCKPEEGLEARGEALGLVGAOPATEEOEAASSST
LVEVTIGEVPAAESPPOSPQASISLPTMNYPLMSQSYEDSSNOEEGSPTEPDLE
SERQALSRKVAELVHFLLLKYRAREPVTAKMLGSVVGWQYFFPVIFSKASSLQL
VFGIELMEVDPIGHLVIFATCIGLSYDGLGDNQIMPKAGLLIIVLAIAREGDCAPE
EKIWEELSVLEVEFEGREDSILGDPKKLLTQHVFQENYLEYRQVPGSDPACYEFLWGPR
ALVETSYVKVYLHHMVKISGGPHISYPPLHEWVLRGEE"
BASE COUNT      411 a      398 c      448 g      406 t
ORIGIN
```

```

Query Match      32.9%; Score 74; DB 9; Length 1663;
Best Local Similarity 99.2%; Pred. No. 4.2e-32;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  36  TTCCTTCAGCTGCTCTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  612 TTCCTTCAGCTGCTCTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACTTGT 671
    ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY  96  CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCCTGCTGGGTGACATCAGATCAT 155
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  672 CATCTTTGCCACCTGCCTGGGCCCTCTCCTACGATGGCCTGCTGGGTGACATCAGATCAT 731
    ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY  156 GCCCA 160
    |||||
Db  732 GCCCA 736
```

Search completed: May 9, 2002, 23:44:07
Job time: 7999 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2002, 22:39:08 ; Search time 257.01 Seconds
(without alignments)
1503.077 Million cell updates/sec

Title: US-08-037-230D-18

Perfect score: 225

Sequence: 1 TATTTCCTTCCTGATCTT.....CGGACTGTGCCCTGAGGAG 225

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_032802.*

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	225	100.0	225	13	AAQ32362
2	225	100.0	225	15	AAQ72487
3	225	100.0	225	20	AAQ84122
4	174	77.3	225	16	AAQ701166
5	157	69.8	1362	20	AAQ87596
6	157	69.8	1375	19	AAV22716
7	157	69.8	4204	22	AAQ20556
8	74	32.9	666	22	AAQ18141
9	74	32.9	945	22	AAQ12993

10	74	32.9	1212	20	AAQ87592
11	74	32.9	1353	20	AAQ87588
12	74	32.9	1640	15	AAQ72480
13	74	32.9	1640	20	AAQ84116
14	74	32.9	4204	20	AAQ26974
15	74	32.9	4204	21	AAQ37927
16	74	32.9	4204	22	AAQ18140
17	69	30.7	379	18	AAQ63345
18	69	30.7	1640	13	AAQ32355
19	56	24.9	268	18	AAQ63347
20	56	24.9	376	18	AAQ63346
21	49	21.8	271	18	AAQ63350
22	49	21.8	378	18	AAQ63349
23	43	19.1	271	18	AAQ63348
24	36	16.0	727	22	AAQ21285
25	36	16.0	920	22	ABA36364
26	36	16.0	920	22	AAQ24300
27	36	16.0	920	22	AAQ49576
28	36	16.0	1956	22	ABA26487
29	36	16.0	1956	22	AAQ15118
30	36	16.0	1956	22	AAQ36453
31	36	16.0	4157	13	AAQ32353
32	36	16.0	4157	15	AAQ72478
33	36	16.0	4157	20	AAQ84114
34	27	12.0	27	15	AAQ44759
35	27	12.0	27	17	AAQ35415
36	26	11.6	26	20	AAQ28066
37	26	11.6	1030	22	AAQ21286
38	26	11.6	4523	22	AAQ06131
39	24	10.7	24	16	AAQ05085
40	24	10.7	24	21	AAQ35541
41	24	10.7	24	22	AAQ84241
42	24	10.7	24	22	AAQ67098
43	24	10.7	27	24	ABA81874
44	24	10.7	44	18	AAQ06033
45	23	10.2	31	21	AAQ09232

ALIGNMENTS

RESULT 1

AAQ32362
ID AAQ32362 standard; DNA; 225 BP.

XX AC AAQ32362;

XX DF 22-APR-1993 (first entry)

XX DE MAGE-6 gene.

XX KW Melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.

XX OS Homo sapiens.

XX PN WO9220356-A.

XX PD 26-NOV-1992.

XX PF 22-MAY-1992; 92WO-US04354.

XX PR 23-MAY-1991; 91US-0705702.

XX PR 09-JUL-1991; 91US-0728838.

XX PR 23-SEP-1991; 91US-0764364.

XX PR 12-DEC-1991; 91US-0807043.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;

XX Van Den Eynde B, Van Der Bruggen P, Van Pel A;

XX WPI; 1992-415460/50.

XX Nucleic acid mol. encoding a human tumour rejection antigen precursor - useful as an immunostimulant in a vaccine for treating and preventing cancers, also useful in diagnosis

XX Disclosure; Page 88; 142pp; English.

XX The sequences given in AAQ32352-69 represent a new family of genes referred to as melanoma antigens (MAGE). The cDNAs of this gene family were identified during the isolation of the antigen E gene. The MAGE cDNAs, when tested, did not transfer expression of antigen E, but they did show substantial homology to the antigen E cDNA sequence. The MAGE DNAs share a certain degree of homology with each other and are expressed in tumour cells including several types of human tumour cells as well as in human tumors. MAGE expression is not restricted to melanomas. MAGE refers to a family of tumor rejection antigen precursors. The antigens resulting from these genes are referred to as MAGE TRAS or melanoma antigen tumor rejection antigens. See also AAQ32351.

XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 13; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.1e-105;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTCTTCTGATCTTCAGCAAGCTCCGATTCCTTGCGAGCTGCTTTGGCATC 60
DB 1 TATTCTTCTGATCTTCAGCAAGCTCCGATTCCTTGCGAGCTGCTTTGGCATC 60

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGGCAGCTGCTGGGCTC 120
DB 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGGCAGCTGCTGGGCTC 120

QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCCAGGACAGCTTCTGTATATC 180
DB 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCCAGGACAGCTTCTGTATATC 180

QY 181 ATCTTGCCCATATTCGCAAGAGGGGAGCTGTGCCCTGAGGAG 225
DB 181 ATCTTGCCCATATTCGCAAGAGGGGAGCTGTGCCCTGAGGAG 225

RESULT 2
AAQ72487
ID AAQ72487 standard; cDNA to mRNA; 225 BP.
XX AC AAQ72487;
XX 22-JUN-1995 (first entry)
XX Tumour rejection antigen MAGE-6 cDNA.
XX Tumour rejection antigen; melanoma antigen-6; MAGE-6; MAGE-3;
XX cancer; cytolytic T cells; antigen D; human leucocyte antigen; ss.
XX Homo sapiens.
XX WO9423031-A.
XX 13-OCT-1994.
XX 17-MAR-1994; 94WO-US02877.
XX 26-MAR-1993; 93US-0037230.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Boon-falleur T, Gaugler B, Van Den EYNDE B, Van DER BRUGGEN P;
XX WPT; 1994-333192/41.

XX New tumour rejection antigen precursor MAGE3 - useful in treatment and diagnosis of cancer

XX Example 32; Page 73; 105pp; English.

XX AAQ72487 is the cDNA sequence which codes for melanoma antigen-6 (MAGE-6). Another melanoma antigen MAGE-3 is encoded by AAQ72470, this is a tumour rejection antigen precursor. Melanomas characterised by the expression of MAGE-3 can be detected, or monitored, by contacting a test sample with an agent that can recognise MAGE-3. The melanoma can be treated by the administration of cytolytic T cells specific for the complex of antigen D (the mature rejection antigen derived from MAGE-3) and a human leucocyte antigen (esp. HLA-A1).

XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 15; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.1e-105;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTCTTCTGATCTTCAGCAAGCTCCGATTCCTTGCGAGCTGCTTTGGCATC 60
DB 1 TATTCTTCTGATCTTCAGCAAGCTCCGATTCCTTGCGAGCTGCTTTGGCATC 60

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGGCAGCTGCTGGGCTC 120
DB 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGGCAGCTGCTGGGCTC 120

QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCCAGGACAGCTTCTGTATATC 180
DB 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCCAGGACAGCTTCTGTATATC 180

QY 181 ATCTTGCCCATATTCGCAAGAGGGGAGCTGTGCCCTGAGGAG 225
DB 181 ATCTTGCCCATATTCGCAAGAGGGGAGCTGTGCCCTGAGGAG 225

RESULT 3
AAQ84122
ID AAX84122 standard; cDNA; 225 BP.
XX AC AAX84122;
XX 08-SEP-1999 (first entry)
XX MAGE-6 gene.
XX Tumour rejection antigen; vaccine; cancer; MAGE-6 gene; ss.
XX Homo sapiens.
XX US5925729-A.
XX 20-JUL-1999.
XX 02-MAY-1994; 94US-0142368.
XX 02-MAY-1994; 94US-0142368.
XX 23-MAY-1991; 91US-0705702.
XX 09-JUL-1991; 91US-0728838.
XX 23-SEP-1991; 91US-0764365.
XX 12-DEC-1991; 91US-0807043.
XX (LUDW-) LUDWIG INST CANCER RES.
XX Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
XX Van Den EYNDE B, Van Der Bruggen P, Van Pel A;
XX WPT; 1999-418294/35.

PT New tumour rejection antigen is useful as a vaccine against
PT cancerous diseases
XX
PS Disclosure; Column 69-70; 58pp; English.
XX
CC This sequence represents the MAGE-6 gene sequence.
CC The invention relates to a tumour rejection antigen sequence that is
CC useful as a tumour rejection antigen for vaccination against cancerous
CC conditions.
XX
SQ Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 20; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.1e-105;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TATTTCCTCTGATCTTCAGCAAGCTTCGAGTCTCTTGCAGCTGGTCTTTGGCCTC 60
Db 1 tattttctctgtatcttcagcaaaagcttcagattcttgcagctgtctttggcctc 60
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACCTGTACATCTTTGCCACCTGCTGGCCTC 120
Db 61 gagctgatggaagtggaccccatcgccacgtgtacatctttgccacctgacctgagag 120
Qy 121 TCCTACGATGCGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCTGTATAATC 180
Db 121 tcttacctgagcctgctggtggacaatcagatcatgccccagagcaggttctctgataatc 180
Qy 181 ATCTGGCCATTAATCGCAAGAGGGGAGTGTGCCCTCGAGGAG 225
Db 181 atctggccataatcgcaagaggagactgtgccccctgaggag 225

RESULT 4
AAT01166
ID AAT01166 standard; DNA; 225 BP.
XX AC AAT01166;
XX
DT 26-FEB-1996 (first entry)
DE MAGE-6 gene.
XX
KW MAGE-6; melanoma; tumour rejection antigen; cancer; diagnosis; ss.
XX Homo sapiens.
XX WO9523874-A1.
XX
PD 08-SEP-1995.
XX
PF 23-FEB-1995; 95WO-US02203.
XX
PR 30-NOV-1994; 94US-0346774.
PR 01-MAR-1994; 94US-0204727.
PR 10-MAR-1994; 94US-0209172.
PR 01-SEP-1994; 94US-0299849.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, Brasseur F, Chomez P, De Plaen E;
PI De Smet C, Gaugler B, Lethe B, Marchand M, Patard J;
PI Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants P;
XX
DR WPI; 1995-320586/41.
XX
PT Determn. of cancerous condition(s) - using a nucleic acid as a
PT primer to determine expression of a MAGE tumour rejection antigen
PT precursor
XX
PS Example 32; Page 80; 121pp; English.
XX

CC A family of human tumour rejection antigen precursor, MAGE, genes
CC (AAT0591-99, AAT01165-71) was isolated from various tumour cell lines.
CC cDNA (AAT01166) coding for MAGE-6 was obtd. from human melanoma
CC LB-33-MEL cells. MAGE serve as markers for tumour diagnosis. The
CC genes are silent in normal cells.
XX
SQ Sequence 225 BP; 44 A; 66 C; 57 G; 58 T; 0 other;

Query Match 77.3%; Score 174; DB 16; Length 225;
Best Local Similarity 99.6%; Pred. No. 3.6e-79;
Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TATTTCCTCTGATCTTCAGCAAGCTTCGAGTCTCTTGCAGCTGGTCTTTGGCCTC 60
Db 1 tattttctctgtatcttcagcaaaagcttcagattcttgcagctgtctttggcctc 60
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACCTGTACATCTTTGCCACCTGCTGGCCTC 120
Db 61 gagctgatggaagtggaccccatcgccacgtgtacatctttgccacctgacctggcctc 120
Qy 121 TCCTACGATGCGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCTGTATAATC 180
Db 121 tcttacctgagcctgctggtggacaatcagatcatgccccagagcaggttctctgataatc 180
Qy 181 ATCTGGCCATTAATCGCAAGAGGGGAGTGTGCCCTCGAGGAG 225
Db 181 atctggccataatcgcaagaggagactgtgccccctgaggag 225

RESULT 5
AAX87596
ID AAX87596 standard; cDNA; 1362 BP.
XX AC AAX87596;
XX
DT 26-OCT-1999 (first entry)
DE CLYTA-MAGE-3-His fusion DNA.
XX
KW MAGE-3; CLYTA-MAGE-3-His; fusion protein; tumour; melanoma;
KW breast cancer; bladder cancer; lung cancer; colon cancer;
KW head and squamous cell carcinoma; oesophagus carcinoma; vaccine;
KW human; ss.
XX
OS Chimeric - Streptococcus pneumoniae.
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
PN WO9940188-A2.
XX
PD 12-AUG-1999.
XX
PF 02-FEB-1999; 99WO-EP00660.
XX
PR 06-FEB-1998; 98GB-0002650.
PR 05-FEB-1998; 98GB-0002543.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX
DR WPI; 1999-494293/41.
DR P-PSDB; AAY06593.
XX
PT New protein derivatives used in cancer vaccine therapy for treating
PT a range of cancers including melanomas, carcinomas and cancers of
PT breast
XX
PS Example 10; Page 72; 72pp; English.
XX
CC This DNA sequence codes for a fusion protein (see AAY06593) composed
CC of the C-terminal portion of the Streptococcus pneumoniae LYTA

CC protein (CLYTA), the human MAGE-3 tumour-associated antigen and a
 CC hexahistidine tail. A vector designed for recombinant expression
 CC of the fusion protein in Escherichia coli is provided. The CLYTA
 CC moiety provides expression of soluble fusion protein, facilitates
 CC affinity purification of the fusion protein, and also acts as a
 CC T-helper epitope. The invention relates to MAGE proteins fused to
 CC an immunological fusion partner, e.g. CLYTA-MAGE-3-His. These novel
 CC fusion proteins provide vaccines for immunotherapy of melanomas or
 CC other MAGE-associated tumours like breast, bladder, lung and
 CC non-small cell lung cancer, head and squamous cell carcinoma, colon
 CC carcinoma and oesophagus carcinoma.
 XX
 SQ Sequence 1362 BP; 345 A; 348 C; 383 G; 286 T; 0 other;

Query Match 59.8%; Score 157; DB 20; Length 1362;
 Best Local Similarity 100.0%; Pred. No. 1.8e-70;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACGTGGTCTTTGGCATCGAG 63
 DB 826 ttcttctctgtatcttcagcaagcttcgattccttgagctggcttttggcatcgag 885
 QY 64 CTGATGGAAGTGGACCCCATCGGACGTGTACATCTTTGCCACTGCCTGGGCTCTCC 123
 DB 886 ctgatggaagtggaccccatcgccacgtgtacatctttgacacctgcctgggctctcc 945
 QY 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
 DB 946 taccatggcctgctgggtgacaaatcagatcatgccca 982

RESULT 6
 AAV22716
 ID AAV22716 standard; DNA; 1375 BP.
 XX
 AC AAV22716;
 XX
 DT 18-AUG-1998 (first entry)
 XX
 DE MAGE-6 cDNA.
 XX
 KW Human tumor rejection antigen precursor; TRA; MAGE-6; HLA-Cw*16;
 KW major histocompatibility complex; MHC; cytotoxic T-cell; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9810780-A1.
 XX
 PD 19-MAR-1998.
 XX
 PF 27-AUG-1997; 97WO-US15069.
 XX
 PR 13-SEP-1996; 96US-0713354.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Bocrn-Falleur T, Deplaen E, Van Der Bruggen P;
 PI
 XX WPI: 1998-207144/18.
 XX

XX Tumour rejection antigen precursor, MAGE-6 derived peptide(s) which
 PT bind to HLA-Cw*16 - used for provoking proliferation of cytotoxic T
 PT cells, useful for, e.g. treatment of cancerous cells
 XX
 PS Disclosure; Page 19; 31pp; English.
 XX
 CC The present sequence represents a MAGE-6 cDNA encoding a human tumor
 CC rejection antigen (TRA) precursor. The invention provides for TRAs
 CC (AAW56268-W56272) which are processed from TRA precursors that are
 CC derived from the MAGE-6 gene. The TRAs bind to major histocompatibility
 CC complex (MHC) molecules of the type HLA-Cw*16 to provoke a cytotoxic
 CC T-cell response against cells exhibiting this particular TRA-MHC

CC complex. As the cells presenting these complexes are human cancerous
 CC cells, the TRA peptides are claimed to be useful in provoking lysis of
 CC these cancerous cells thereby providing a probable method of treating
 CC cancer.
 XX
 SQ Sequence 1375 BP; 293 A; 364 C; 404 G; 314 T; 0 other;

Query Match 59.8%; Score 157; DB 19; Length 1375;
 Best Local Similarity 100.0%; Pred. No. 1.8e-70;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACGTGGTCTTTGGCATCGAG 63
 DB 595 ttcttctctgtatcttcagcaagcttcgattccttgagctggcttttggcatcgag 654
 QY 64 CTGATGGAAGTGGACCCCATCGGACGTGTACATCTTTGCCACTGCCTGGGCTCTCC 123
 DB 655 ctgatggaagtggaccccatcgccacgtgtacatctttgacacctgcctgggctctcc 714
 QY 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
 DB 715 tacyatggcctgctgggtgacaaatcagatcatgccca 751

RESULT 7
 AAS02056
 ID AAS02056 standard; CDNA; 4204 BP.
 XX
 AC AAS02056;
 XX
 DT 16-JUL-2001 (first entry)
 XX
 DE DNA encoding molecule for disease detection and treatment, mddt21.
 XX
 KW Human; mddt21; gene therapy; adenosine deaminase deficiency;
 KW ADA; severe combined immunodeficiency syndrome; cystic fibrosis;
 KW thalassaemia; familial hypercholesterolaemia; haemophilia; factor VIII;
 KW factor IX; cancer; cell proliferation; parasite; human retrovirus; HIV;
 KW hepatitis B; hepatitis C; Candida albicans; Plasmodium falciparum;
 KW Paracoccidioides brasiliensis; Trypanosoma brasiliensis; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200123538-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 22-SEP-2000; 2000WO-US26085.
 XX
 PR 28-SEP-1999; 99US-0156565.
 PR 30-NOV-1999; 99US-0168197.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;
 PI Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS;
 PI Hillman JL, Jones AL, Yu JY, Greenawalt LB, Panzer SR;
 PI Roseberry AM, Wright RJ, Chen W, Liu TF, Yap PE, Stockdreher TK;
 PI Anshey S, Fong WT;
 XX
 XX WPI: 2001-258131/26.

XX Purified disease treatment and detection molecule polynucleotides and
 XX polypeptides, useful for providing diagnostic assays and gene therapy -
 PS Claim 1; Page 109-110; 113pp; English.
 XX

XX The sequence represents the coding sequence of molecule for disease
 CC detection and treatment, mddt21, shown by computer analysis to be similar
 CC to the MAGE family of proteins. The sequence may be used for
 CC somatic or germline gene therapy. Gene therapy may be performed to: (i)
 CC correct genetic deficiency such as in severe combined immunodeficiency

CC syndrome associated with adenosine deaminase (ADA) deficiency, cystic
CC fibrosis, thalassaemias, familial hypercholesterolaemia and haemophilia
CC caused by factor VIII or factor IX deficiencies; (ii) express a
CC conditional lethal gene product (such as in the case of cancers which
CC result from unregulated cell proliferation); (iii) express a protein
CC which affords protection against intracellular parasites (for example,
CC human retroviruses such as HIV, hepatitis B or C, fungal parasites such
CC as Candida albicans and Paracoccidioides brasiliensis, and protozoal
CC parasites such as Plasmodium falciparum and Trypanosoma brasiliensis.
XX
SQ Sequence 4204 BP; 947 A; 1145 C; 1219 G; 893 T; 0 other;

Query Match 69.8%; Score 157; DB 22; Length 4204;
Best Local Similarity 100.0%; Pred. No. 1.9e-70;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCGAGCTGGTCTTGGCATCGAG 63
DB 2900 ttcttctctgtgatcttcagcaagcttcgagattcccttgagctggtctttggcatcgag 2959
|||||
QY 64 CTGATGAAGTGGACCCATCGGCGACGTGTACATCTTTGGCACCTGCCTGGGCTCTCC 123
DB 2960 ctgatggaagtggaccccatcgccacgtgtacatctttggccacctgctgggacctcc 3019
|||||
QY 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCA 160
DB 3020 tacgatggcctgctgggtgacaaatcagatcatgccca 3056
|||||
RESULT 8
AAD18141
ID AAD18141 standard; cDNA; 666 BP.
XX
AC AAD18141;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human melanoma associated antigen 3 (MAGE-3) truncated cDNA.
XX
KW Human; melanoma associated antigen 3; MAGE-3; neuroprotective; neurotropic;
KW immunosuppressive; caspase-12 activation; cell death related disease;
KW cell death inhibitor; cancer-specific protein; Alzheimer's disease;
KW neurodegenerative disease; autoimmune disease; anyotrophy; gene therapy;
KW organ disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..666
FT /*tag= a
FT /product= "Human MAGE-3 protein"
FT /note= "CDS does not include start codon"
FT /partial
XX
PN EPI126027-A1.
XX
XX 22-AUG-2001.
XX
PF 16-FEB-2001; 2001EP-0301361.
XX
PR 18-FEB-2000; 2000JP-0041927.
XX
XX (RIKE) RIKEN KK.
XX
PI Morishima N, Shibata T;
XX
DR WPI; 2001-591501/67.
DR P-PSDB; AAE10673.
XX
XX New polypeptide for treating cell death related diseases such as
PT Alzheimer's disease, neurodegenerative diseases, autoimmune diseases,
PT anyotrophy and organ disorders comprises the recombinant

PT cancer-specific protein MAGE-3 -
XX
PS Claim 3; Page 25-27; 41pp; English.
XX
CC The present sequence is the truncated form of human melanoma
CC associated antigen 3 (MAGE-3) cDNA. The present invention relates
CC to MAGE-3 protein or its truncated form which specifically bind to
CC caspase-12 or pro-caspase-12 protein and inhibit their activation.
CC MAGE-3 proteins are cancer-specific proteins and are used as cell-
CC death inhibitors. Therapeutic agents comprising MAGE-3 sequence are
CC useful for treating cell death related diseases such as Alzheimer's
CC disease, neurodegenerative diseases, autoimmune diseases, anyotrophy
CC and organ disorders. MAGE-3 gene is useful as an agent for gene therapy.
CC The sequences of the invention are useful for preventing or treating a
CC cell death-related disease developing in tissues in the nervous system,
CC vascular system, respiratory system, digestive system, lymph system,
CC urinary system, or reproductive system.
XX
SQ Sequence 666 BP; 151 A; 165 C; 197 G; 153 T; 0 other;

Query Match 32.9%; Score 74; DB 22; Length 666;
Best Local Similarity 99.2%; Pred. No. 4.8e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTGCGAGCTGGTCTTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCGCATGTA 95
DB 189 ttcttgcagctggtcttttggcatcgagctgataagtgaccccatcgccacttgta 248
|||||
QY 96 CATCTTTGCCACCTGCGCTGGGCGCTCTCTACGATGGCCTGTGGTGACATCATCAT 155
DB 249 catctttgccacctgctggcgctctctctacgagtgctgctgggtgacatcatcat 308
|||||
QY 156 GCCCA 160
DB 309 gccca 313
|||||

RESULT 9
AAD12993
ID AAD12993 standard; DNA; 945 BP.
XX
AC AAD12993;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human MAGE-A3 DNA.
XX
KW MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;
KW tumour cell; immunostimulant; antigen presentation; cancer; melanoma;
KW CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;
KW myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic;
KW gene therapy; human; MAGE-A3; tumour rejection antigen; TRA; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..945
FT /*tag= a
FT /product= "MAGE-A3 protein"
XX
PN WO200153833-A1.
XX
PD 26-JUL-2001.
XX
PF 19-JAN-2001; 2001WO-US02008.
XX
PR 20-JAN-2000; 2000US-0177242.
PR 25-OCT-2000; 2000US-0243212.
XX
FA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Luiten R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;

PI Demotte N, Schultz E;
XX
DR WPI: 2001-488724/53.
DR P-PSDB; AAE06853.

XX Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or
PT HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used
PT in diagnosis and treatment of a disorder characterized by expression of
PT MAGE-A1 or -A3 -
XX

PS Example 3; Page 94-95; 103pp; English.

XX The invention relates to functional variants and isolated mimetics of a
CC MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide,
CC or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described
CC in the specification. MAGE genes encode tumour rejection antigens
CC (TRAS) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules.
CC The MAGE antigenic peptide acts by binding to HLA molecules
CC on tumour cells and stimulating recognition of these cells and thus
CC signalling them to the immune system for destruction. The peptide when
CC presented by HLA molecule induces the activation and stimulation of
CC CD4+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to
CC treat and diagnose disorders characterised by expression of MAGE-A1
CC or -A3. Disorders include cancers e.g melanomas, oesophageal, lung,
CC head and neck, breast, colorectal, prostate, renal, bladder,
CC hepatocellular, papillary thyroid and gastric carcinomas, myelomas,
CC brain tumours, sarcomas, seminomas, and ovarian tumours. The present
CC sequence is human MAGE-A3 DNA.

XX Sequence 945 BP; 210 A; 254 C; 278 G; 203 T; 0 other;

Query Match 32.9%; Score 74; DB 22; Length 945;
Best Local Similarity 99.2%; Pred. No. 4.9e-28; Length 945;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 36 TTCCTTCGAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGCTGTA 95
Db 468 ttccttgagctgtgtcttggcatcgagctgagtggaagtgaacccatcgccactgtga 527
Qy 96 CATCTTTGCCACCTGCGCCCTCTCTACGATGGCTGCTGGTGACATCAGATCAT 155
Db 528 catctttgccacctgctggcctctctctacgatggcctgctggtgacaatcagatcat 587

Qy 156 GCCCA 160
Db 588 gccca 592

RESULT 10
AAX87592
ID AAX87592 standard; cDNA; 1212 BP.

XX AAX87592;

XX 26-OCT-1999 (first entry)

XX Haemagglutinin-MAGE-3-His fusion DNA.

XX MAGE-3; haemagglutinin; NSI-MAGE-3-His; fusion protein; tumour;
KW melanoma; breast cancer; bladder cancer; lung cancer;
KW head and squamous cell carcinoma; colon cancer;
KW oesophagus carcinoma; vaccine; human; ss.

XX Chimeric - Influenza virus.
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.

XX WO9940188-A2.

XX 12-AUG-1999.

XX 02-FEB-1999; 99WO-EP00660.

XX 06-FEB-1998; 98GB-0002650.
PR 05-FEB-1998; 98GB-0002543.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Cabazon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;

XX WPI: 1999-494293/41.

DR P-PSDB; AAY06591.

XX New protein derivatives used in cancer vaccine therapy for treating
PT a range of cancers including melanomas, carcinomas and cancers of
PT breast

XX Example 7; Page 69; 72pp; English.

XX This DNA sequence codes for a fusion protein (see AAY06591) composed
CC of haemagglutinin NSI of influenza virus, the human MAGE-3
CC tumour-associated antigen and a hexahistidine tail. A vector
CC designed for recombinant expression of the fusion protein is
CC provided. MAGE-3 cDNA was amplified using primers that altered the
CC first 5 codons to Escherichia coli codon usage. The NSI moiety
CC provided the fusion protein with additional exogenous T-helper
CC epitopes. The invention relates to MAGE proteins fused to an
CC immunological fusion partner, e.g. NSI-MAGE-3-His. These novel
CC fusion proteins provide vaccines for immunotherapy of melanomas or
CC other MAGE-associated tumours like breast, bladder, lung and
CC non-small cell lung cancer, head and squamous cell carcinoma, colon
CC carcinoma and oesophagus carcinoma.

XX Sequence 1212 BP; 289 A; 319 C; 344 G; 260 T; 0 other;

Query Match 32.9%; Score 74; DB 20; Length 1212;
Best Local Similarity 99.2%; Pred. No. 4.9e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 36 TTCCTTCGAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGCTGTA 95
Db 708 ttccttgagctgtgtcttggcatcgagctgagtggaagtgaacccatcgccactgtga 767
Qy 96 CATCTTTGCCACCTGCGCCCTCTCTACGATGGCTGCTGGTGACATCAGATCAT 155
Db 768 catctttgccacctgctggcctctctctacgatggcctgctggtgacaatcagatcat 827

Qy 156 GCCCA 160
Db 828 gccca 832

RESULT 11
AAX87588
ID AAX87588 standard; cDNA; 1353 BP.

XX AAX87588;

XX 26-OCT-1999 (first entry)

XX Lipoprotein D-MAGE-3-His fusion DNA.

XX MAGE-3; lipoprotein D; LPD-MAGE-3-His; fusion protein; tumour;
KW melanoma; breast cancer; bladder cancer; lung cancer;
KW head and squamous cell carcinoma; colon cancer;
KW oesophagus carcinoma; vaccine; human; ss.

XX Chimeric - Haemophilus influenzae.
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.

XX WO9940188-A2.

XX 12-AUG-1999.

```

XX 02-FEB-1999; 99WO-EP00660.
XX 06-FEB-1998; 98GB-0002650.
XX 05-FEB-1998; 98GB-0002543.
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX Cabazon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX WPI; 1999-494293/41.
XX P-PSDB; AAY06589.
XX New protein derivatives used in cancer vaccine therapy for treating
XX a range of cancers including melanomas, carcinomas and cancers of
XX breast
XX Example 1; Page 66; 72pp; English.
XX This DNA sequence codes for a fusion protein (see AAY06589) composed
XX of lipidated protein D (LPD) of Haemophilus influenzae B, the human
XX MAGE-3 tumour-associated antigen and a hexahistidine tail. A
XX vector designed for recombinant expression of the fusion protein is
XX provided. MAGE-3 cDNA was amplified using primers that altered the
XX first 5 codons to Escherichia coli codon usage. The LPD moiety
XX provided the fusion protein with additional exogenous T-cell
XX epitopes and also increased expression levels in E. coli. The
XX lipid tail ensured optimal presentation of the antigen to
XX antigen-presenting cells. The affinity tag facilitated
XX purification. The invention relates to MAGE-3-His. These novel
XX immunological fusion partner, e.g. LPD-MAGE-3-His. These novel
XX fusion proteins provide vaccines for immunotherapy of melanomas or
XX other MAGE-associated tumours like breast, bladder, lung and
XX non-small cell lung cancer, head and squamous cell carcinoma, colon
XX carcinoma and oesophagus carcinoma.
XX Sequence 1353 BP; 342 A; 337 C; 354 G; 320 T; 0 other;

Query Match 32.9%; Score 74; DB 20; Length 1353;
Best Local Similarity 99.2%; Pred. No. 4.9e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTCGAGCTGCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95.
Db 849 ttccttcgagctgctcttggcatcgagctgagtggaagtggaaccccatcgccactgtga 908

QY 96 CATCTTTGCCACCTGCTTGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
Db 909 catctttgccacctgcttggccctctctctacgatggcctgctgggtgacaatcagatcat 968

QY 156 GCCCA 160
Db 969 gccca 973

RESULT 12
AAQ72480
ID AAQ72480 standard; cDNA to mRNA; 1640 BP.
XX
XX AC AAQ72480;
XX
XX 22-JUN-1995 (first entry)
XX Tumour rejection antigen precursor MAGE-3 cDNA.
XX Tumour antigen rejection precursor; melanoma antigen-3; MAGE-3;
XX cancer; cytolytic T cells; antigen D; human leucocyte antigen;
XX PIA gene; ss.
XX Homo sapiens.
XX Key Location/Qualifiers

```

```

FT CDS 172..1116
FT FT /*tag= a
XX
XX PN WO9423031-A.
XX
XX PD 13-OCT-1994.
XX
XX PF 17-MAR-1994; 94WO-US02877.
XX
XX PR 26-MAR-1993; 93US-0037230.
XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX PI Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
XX WPI; 1994-333192/41.
XX
XX PT New tumour rejection antigen precursor MAGE3 - useful in
XX treatment and diagnosis of cancer
XX
XX PS Example 32; Page 64; 105pp; English.
XX
XX CC AAQ72480 is the P1A gene fragment which contains the cDNA coding
XX sequence AAQ72470, which encodes melanoma antigen-3 (MAGE-3), a tumour
XX rejection antigen precursor. Melanomas characterised by the expression of
XX MAGE-3 can be detected, or monitored, by contacting a test sample with
XX an agent that can recognise MAGE-3. The melanoma can be treated by the
XX administration of cytolytic T cells specific for the complex of
XX antigen D (the mature rejection antigen derived from MAGE-3) and a
XX human leucocyte antigen (esp. HLA-A1).
XX
XX SQ Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;

Query Match 32.9%; Score 74; DB 15; Length 1640;
Best Local Similarity 99.2%; Pred. No. 4.9e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCCTTCGAGCTGCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
Db 639 ttccttcgagctgcttggcatcgagctgagtggaagtggaaccccatcgccactgtga 698

QY 96 CATCTTTGCCACCTGCTTGGCCCTCTCCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
Db 699 catctttgccacctgcttggccctctctctacgatggcctgctgggtgacaatcagatcat 758

QY 156 GCCCA 160
Db 759 gccca 763

RESULT 13
AAQ84116
ID AAQ84116 standard; cDNA to mRNA; 1640 BP.
XX
XX AC AAQ84116;
XX
XX DT 08-SEP-1999 (first entry)
XX
XX DE MAGE-3 gene.
XX
XX KW Tumour rejection antigen; vaccine; cancer; MAGE-3 gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN US5925729-A.
XX
XX PD 20-JUL-1999.
XX
XX PF 02-MAY-1994; 94US-0142368.
XX
XX PR 02-MAY-1994; 94US-0142368.
XX 23-MAY-1991; 91US-0705702.

```


DR P-PSDB; AAB02565.
XX
PT New MAGE-A3 class II binding peptides, useful to diagnose and treat
PT tumours, are fragments of MAGE-A3 which bind to and are presented to T
PT lymphocytes by human leukocyte antigen class II molecules
XX
PS Example 6; Page 96-98; 119pp; English.
XX
CC The present invention relates to MAGE-A3 (tumour associated gene
CC product) human leukocyte antigen (HLA) class II-binding peptides (see
CC AAB02566-B02595, and AAB02633-B02637). These peptides are presented to T
CC cells in the context of HLA class II molecules. The peptides stimulate
CC the activity and proliferation of CD4+ T lymphocytes. The invention also
CC includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928
CC and AAA37938-A37940). The peptides and nucleotide sequences can be used
CC to create antibodies against the MAGE-A3 peptides, the antibodies,
CC peptides and nucleotide sequences can be used to create a vaccine. The
CC peptides are used to diagnose or treat a disorder characterized by
CC expression of MAGE-3, particularly cancer. The methods can also be used
CC in the diagnosis of disorders associated with MAGE-3 expression. Included
CC in the invention are other human tumour antigens (see AAB02596-B02637),
CC and PCR primers used in the course of the invention (see AAA37929-A37937
CC and AAA37941-A37942).
XX
SQ Sequence 4204 BP; 944 A; 1144 C; 1223 G; 893 T; 0 other;

Query Match 32.9%; Score 74; DB 21; Length 4204;
Best Local Similarity 99.2%; Pred. No. 5e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 36 TTCCTTCGACGTGCTCTTTGGCATCGAGCTGATGGAGTGGACCCCATCGGCCACGTGTA 95
Db 2932 ttccttcgacgtgtcttggcatcgagctgatggagtgagcccatcgccacttgta 2991
QY 96 CATCTTTGCCACCTGCTGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
Db 2992 catctttgccacctgctggccctctctctacgatggcctgctggtgacaatcagatcat 3051
QY 156 GCCCA 160
Db 3052 gccca 3056

Search completed: May 9, 2002, 23:49:42
Job time: 4234 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2002, 21:24:18 ; Search time 1791.78 Seconds
(without alignments)
1694.859 Million cell updates/sec

Title: US-08-037-230D-18
Perfect score: 225
Sequence: 1 TATTTCCTTCCTGATCTT.....GCGACTGTCCTCGAGGAG 225

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*

- 1: em_estba:**
- 2: em_esthum:**
- 3: em_estin:**
- 4: em_estmu:**
- 5: em_estov:**
- 6: em_estpl:**
- 7: em_estro:**
- 8: em_htc:**
- 9: gb_estl:**
- 10: gb_est2:**
- 11: gb_htc:**
- 12: gb_gss:**
- 13: em_gss_hum:**
- 14: em_gss_inv:**
- 15: em_gss_pin:**
- 16: em_gss_vrt:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	69.8	563	10	BG477228
2	157	69.8	768	10	BI086876
3	157	69.8	776	10	BG476912
4	157	69.8	878	10	BG397171
5	157	69.8	886	10	BG476078
6	157	69.8	894	10	BG765817
7	137	60.9	707	10	BG760839
8	137	60.9	876	10	BF792356
9	128	56.9	1021	10	BM470991
10	108	48.0	795	10	BE341476
11	104	46.2	696	10	BE733003
12	102	45.3	704	10	BG764972
13	101	44.9	760	10	BE730893
14	98	43.6	1101	10	BE734462
15	93	41.3	788	10	BG718421
16	93	41.3	929	10	BE275276
17	84	37.3	738	10	BE900916

18	84	37.3	750	10	BE890259
19	84	37.3	1109	10	BG333682
20	83	36.9	683	10	BE407664
21	77	34.2	710	10	BM011988
22	77	34.2	956	10	BE900736
23	74	32.9	623	10	BF793889
24	74	32.9	686	10	BG575715
25	74	32.9	704	10	BI090658
26	74	32.9	769	10	BG765526
27	74	32.9	872	10	BM449726
28	71	31.6	845	10	BI089076
29	69	30.7	767	10	BI092532
30	68	30.2	803	10	BM015882
31	65	28.9	948	9	AL526721
32	64	28.4	810	9	AL526639
33	59	26.2	633	10	BE732114
34	59	26.2	809	10	BI855745
35	56	24.9	845	10	BG481937
36	55	24.4	721	10	BG481226
37	55	24.4	751	10	BE732549
38	55	24.4	816	10	BI086919
39	55	24.4	844	10	BE902106
40	53	23.6	721	10	BM015284
41	52	23.1	740	10	BE727711
42	52	23.1	766	10	BE615115
43	51	22.7	934	10	BG280738
44	50	22.2	597	10	BE281072
45	50	22.2	683	10	BE799994

ALIGNMENTS

RESULT 1
BG477228
LOCUS
602524237F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642641 5',
mRNA sequence.
ACCESSION
BG477228.1 GI:13409507
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 563)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM411 row: i column: 10
High quality sequence stop: 499.
Location/Qualifiers
1. 563
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4642641"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size: 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 133 a 147 c 162 g 121 t

ORIGIN

Query Match 69.8%; Score 157; DB 10; Length 563;
Best Local Similarity 100.0%; Pred. No. 5.3e-70;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTCAGCTGGTCTTTGGCATCGAG 63
|||||
Db 194 TTCTTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTCAGCTGGTCTTTGGCATCGAG 253
|||||
Qy 64 CTGATGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 123
|||||
Db 254 CTGATGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 313
|||||
Qy 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
|||||
Db 314 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 350
|||||

RESULT 2
BI086876 768 bp mRNA linear EST 20-JUN-2001
LOCUS 602850494F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4992143 5',
mRNA sequence.

ACCESSION BI086876
VERSION BI086876.1 GI:14505206
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 768)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LHAM1010 row: k column: 24
High quality sequence stop: 766.

FEATURES
source
1..768
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4992143"
/cell_line="NIH_MGC_10"
/lab_host="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5 kb. Library prepared by Life Technologies."

BASE COUNT 170 a 227 c 212 g 158 t 1 others
ORIGIN

Query Match 69.8%; Score 157; DB 10; Length 768;
Best Local Similarity 100.0%; Pred. No. 5.6e-70;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTCAGCTGGTCTTTGGCATCGAG 63
|||||

Db 541 TTCTTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTCAGCTGGTCTTTGGCATCGAG 600
Qy 64 CTGATGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 123
|||||
Db 601 CTGATGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 660
|||||
Qy 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
|||||
Db 661 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 697
|||||

RESULT 3
BG476912 776 bp mRNA linear EST 21-MAR-2001
LOCUS 602524881F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642868 5',
mRNA sequence.

ACCESSION BG476912
VERSION BG476912.1 GI:13409178
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 776)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTPP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LHCMI412 row: b column: 21
High quality sequence stop: 747.

FEATURES
source
1..776
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4642868"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 180 a 197 c 232 g 167 t
ORIGIN

Query Match 69.8%; Score 157; DB 10; Length 776;
Best Local Similarity 100.0%; Pred. No. 5.6e-70;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTCAGCTGGTCTTTGGCATCGAG 63
|||||
Db 194 TTCTTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTCAGCTGGTCTTTGGCATCGAG 253
|||||

Qy 64 CTGATGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 123
|||||
Db 254 CTGATGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 313
|||||

Qy 124 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
|||||
Db 314 TACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 350
|||||

```

RESULT 4
BG397171
LOCUS 878 bp mRNA linear EST 12-MAR-2001
DEFINITION 602434130F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:452086 5',
mRNA sequence.
ACCESSION BG397171
VERSION BG397171.1 GI:13290619
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: AFCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1247 row: 1 column: 07
High quality sequence stop: 866.
FEATURES
source
Location/Qualifiers
1..878
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:452086"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

BASE COUNT 197 a 214 c 262 g 205 t
ORIGIN

Query Match 69.8%; Score 157; DB 10; Length 878;
Best Local Similarity 100.0%; Pred. No. 5.8e-70;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTTCAGCTGGTCTTTGGCATCGAG 63
Db 193 TTCCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTTCAGCTGGTCTTTGGCATCGAG 252

Qy 64 CTGATGGAAGTGGACCCATCGGCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 123
Db 253 CTGATGGAAGTGGACCCATCGGCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 312

Qy 124 TACGATGGCTGCTGGGTGACAATCAGATCATGCCCA 160
Db 313 TACGATGGCTGCTGGGTGACAATCAGATCATGCCCA 349

RESULT 5
BG476078
LOCUS 886 bp mRNA linear EST 21-MAR-2001
DEFINITION 602520963F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4639670 5',
mRNA sequence.
ACCESSION BG476078
VERSION BG476078.1 GI:13408357
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: AFCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1247 row: 1 column: 15
High quality sequence stop: 730.
FEATURES
source
Location/Qualifiers
1..886
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4639670"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM1741 row: m column: 11
 High quality sequence stop: 835.

FEATURES

source

Location/Qualifiers
 1. .894
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4869682"
 /clone_lib="NIH_MGC_49"
 /tissue_type="melanotic melanoma, high MDR (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library. I"

BASE COUNT 193 a 252 c 275 g 174 t

ORIGIN

Query Match 69.8%; Score 157; DB 10; Length 894;
 Best Local Similarity 100.0%; Pred. No. 5.8e-70;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCTTTCTCTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTGGCATCGAG 63
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 616 TCTTTCTCTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTGGCATCGAG 675
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 64 CTGATGGAAGTGGACCCCGCCACGCTGACATCTTTGCCACCTGGCTGGCCCTCTCC 123
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 676 CTGATGGAAGTGGACCCCGCCACGCTGACATCTTTGCCACCTGGCTGGCCCTCTCC 735
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 124 TACGATGCCCTGCTGGTGCACATCATGATGCCCA 160
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 736 TACGATGCCCTGCTGGTGCACATCATGATGCCCA 772
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 7

BG760839

LOCUS

DEFINITION 602717006F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4840824 5',
 mRNA sequence.

ACCESSION

BG760839

VERSION

BG760839.1

GI:14071479

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 707)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:<http://image.llnl.gov>

Plate: LLCM1741 row: m column: 11

High quality sequence stop: 835.

FEATURES

source

<http://image.llnl.gov>
 Plate: LLCM1672 row: k column: 01
 High quality sequence stop: 619.

Location/Qualifiers
 1. .707
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4840824"
 /clone_lib="NIH_MGC_49"
 /tissue_type="melanotic melanoma, high MDR (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library. I"

BASE COUNT 145 a 241 c 186 g 135 t

ORIGIN

Query Match 60.9%; Score 137; DB 10; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1e-59;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCTTTCTCTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTGGCATCGAG 63
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 402 TCTTTCTCTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTGGCATCGAG 461
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 64 CTGATGGAAGTGGACCCCGCCACGCTGACATCTTTGCCACCTGGCTGGCCCTCTCC 123
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 462 CTGATGGAAGTGGACCCCGCCACGCTGACATCTTTGCCACCTGGCTGGCCCTCTCC 521
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 124 TACGATGCCCTGCTGGG 140
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 522 TACGATGCCCTGCTGGG 538
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 8

BG792356

LOCUS

DEFINITION 602252896F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4345222 5',
 mRNA sequence.

ACCESSION

BG792356

VERSION

BG792356.1

GI:12097410

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 876)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:<http://image.llnl.gov>

Plate: LLCM9964 row: p column: 23

High quality sequence stop: 780.

Location/Qualifiers

1. .876

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4345222"

/clone_lib="NIH_MGC_84"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 185 a 215 c 248 g 228 t
ORIGIN

Query Match 60.9%; Score 137; DB 10; Length 876;
Best Local Similarity 100.0%; Pred. No. 1.1e-59;
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 CAAGCTTCCGATTCCTTGGCAGCTGGTCTTTGGCATCGAGCTGAGTGAAGTGGACCCCAT 83
|||||
Db 101 CAAGCTTCCGATTCCTTGGCAGCTGGTCTTTGGCATCGAGCTGAGTGAAGTGGACCCCAT 160
|||||
Qy 84 CGGCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCTACGATGGCTGCTGGGTGA 143
|||||
Db 161 CGGCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCTACGATGGCTGCTGGGTGA 220
|||||
Qy 144 CAATCAGATATGCCCA 160
|||||
Db 221 CAATCAGATATGCCCA 237
|||||

RESULT 9
BM470991
LOCUS BM470991 1021 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6478212 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5562971
5', mRNA sequence.
ACCESSION BM470991
VERSION BM470991.1 GI:18520033
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1021)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1293 row: d column: 12
High quality sequence stop: 725.
Location/Qualifiers
1. 1021

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5562971"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT 232 a 290 c 292 g 206 t 1 others
ORIGIN

Query Match 56.9%; Score 128; DB 10; Length 1021;

Best Local Similarity 100.0%; Pred. No. 4.7e-55;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 TTCTTTCTGTCATCTTCAGCAAGCTTCCTCGATTCTCTTGCAGCTGCTCTTTGGCATCGAG 63
|||||
Db 596 TTCTTTCTGTCATCTTCAGCAAGCTTCCTCGATTCTCTTGCAGCTGCTCTTTGGCATCGAG 555
|||||
Qy 64 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 123
|||||
Db 656 CTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 715
|||||
Qy 124 TACGATGG 131
|||||
Db 716 TACGATGG 723
|||||

RESULT 10
BE541476
LOCUS BE541476 795 bp mRNA linear EST 09-AUG-2000
DEFINITION 601067928F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454135 5',
mRNA sequence.

ACCESSION BE541476
VERSION BE541476.1 GI:9770121
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 795)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8438 row: h column: 08
High quality sequence stop: 662.
Location/Qualifiers
1. 795

FEATURES
source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3454135"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.5 kb. Library prepared by Life
Technologies."

BASE COUNT 182 a 199 c 234 g 180 t
ORIGIN

Query Match 48.0%; Score 108; DB 10; Length 795;
Best Local Similarity 100.0%; Pred. No. 8.5e-45;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 TTGGCATCAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCC 112
|||||
Db 238 TTGGCATCAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCC 297
|||||

Qy 113 TGGGCTCTCTTACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 160
|||||
Db 298 TGGGCTCTCTTACGATGGCTGCTGGGTGACAAATCAGATCATGCCCA 345
|||||

RESULT 11

BE733003
LOCUS 601569780F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3844482 5', linear mRNA 696 bp EST 15-SEP-2000

DEFINITION BE733003 mRNA sequence.

ACCESSION BE733003

VERSION BE733003.1 GI:10146995

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 696)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM540 row: P column: 19
High quality sequence stop: 693.

FEATURES
Location/Qualifiers
source 1..696
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3844482"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." 142 a 206 c 204 g 144 t

BASE COUNT 142 a 206 c 204 g 144 t

ORIGIN

Query Match 46.2%; Score 104; DB 10; Length 696;
Best Local Similarity 100.0%; Pred. No. 9.4e-43;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTTTCGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTGTTCGGCATCGAG 63
|||||
Db 560 TTCTTTCGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTGTTCGGCATCGAG 619
|||||

Qy 64 CTGATGGAAGTGGACCCCATCGGCCACCTGTACATCTTTGCCAC 107
|||||
Db 620 CTGATGGAAGTGGACCCCATCGGCCACCTGTACATCTTTGCCAC 663
|||||

RESULT 12

LOCUS BG764972

DEFINITION 602737745F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4863059 5', linear mRNA 704 bp EST 15-MAY-2001

ACCESSION BG764972

VERSION BG764972.1 GI:14075625

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 704)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LCM1724 row: i column: 12
High quality sequence stop: 704.

FEATURES
Location/Qualifiers
source 1..704
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4863059"
/clone_lib="NIH_MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." 145 a 214 c 200 g 145 t

BASE COUNT 145 a 214 c 200 g 145 t

ORIGIN

Query Match 45.3%; Score 102; DB 10; Length 704;
Best Local Similarity 100.0%; Pred. No. 1e-41;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 GGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTG 114
|||||
Db 603 GGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTG 662
|||||

Qy 115 GGCCTCTCTACGATGGCTCTGGTGCATCATCATCATC 156
|||||
Db 663 GGCCTCTCTACGATGGCTCTGGTGCATCATCATCATC 704
|||||

RESULT 13

LOCUS BE730893

DEFINITION 601570013F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3844707 5', linear mRNA 760 bp EST 15-SEP-2000

ACCESSION BE730893

VERSION BE730893.1 GI:10144885

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 760)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LCM541 row: j column: 04
High quality sequence stop: 742.

FEATURES
Location/Qualifiers


```

source
1. .760
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DHI0B (phage-resistant)"
/notes="Organ: placenta; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

BASE COUNT	166 a	220 c	216 g	158 t
ORIGIN				

```

Query Match 44.9%; Score 101; DB 10; Length 760;
Best Local Similarity 100.0%; Pred. No. 3.3e-41;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTCTCTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAG 63
|||||
Db 545 TTCTTCTCTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAG 604
|||||

QY 64 CTGATGAAGTGACCCCATCGGCCACGTGTACATCTTTGC 104
|||||
Db 605 CTGATGAAGTGACCCCATCGGCCACGTGTACATCTTTGC 645
|||||

RESULT 14
BE734462 1101 bp mRNA linear EST 15-SEP-2000
LOCUS 601566241F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841042 5',
DEFINITION mRNA sequence.
ACCESSION BE734462
VERSION BE734462.1 GI:10148454
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LICM532 row: a column: 11
High quality sequence stop: 709.
Location/Qualifiers
1. .1101
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DHI0B (phage-resistant)"
/notes="Organ: placenta; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

BASE COUNT 166 a 220 c 216 g 158 t
ORIGIN

Query Match 44.9%; Score 101; DB 10; Length 760;
Best Local Similarity 100.0%; Pred. No. 3.3e-41;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTCTCTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAG 63
|||||
Db 545 TTCTTCTCTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAG 604
|||||

QY 64 CTGATGAAGTGACCCCATCGGCCACGTGTACATCTTTGC 104
|||||
Db 605 CTGATGAAGTGACCCCATCGGCCACGTGTACATCTTTGC 645
|||||

RESULT 14
BE734462 1101 bp mRNA linear EST 15-SEP-2000
LOCUS 601566241F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841042 5',
DEFINITION mRNA sequence.
ACCESSION BE734462
VERSION BE734462.1 GI:10148454
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LICM532 row: a column: 11
High quality sequence stop: 709.
Location/Qualifiers
1. .1101
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DHI0B (phage-resistant)"
/notes="Organ: placenta; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

BASE COUNT 166 a 220 c 216 g 152 t
ORIGIN

Query Match 41.3%; Score 93; DB 10; Length 768;
Best Local Similarity 100.0%; Pred. No. 4.3e-37;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 CAAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGACCCCAT 83
|||||
Db 649 CAAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGACCCCAT 708
|||||

BASE COUNT 272 a 282 c 344 g 203 t
ORIGIN

Query Match 43.6%; Score 98; DB 10; Length 1101;
Best Local Similarity 100.0%; Pred. No. 1.2e-39;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAGCTGATG 69
|||||
Db 603 CCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAGCTGATG 662
|||||

QY 70 GAAGTGACCCCATCGGCCACGTGTACATCTTTGGCCAC 107
|||||
Db 663 GAAGTGACCCCATCGGCCACGTGTACATCTTTGGCCAC 700
|||||

RESULT 15
BG718421 768 bp mRNA linear EST 08-MAY-2001
LOCUS 602696451F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828429 5',
DEFINITION mRNA sequence.
ACCESSION BG718421
VERSION BG718421.1 GI:13997608
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10746 row: f column: 14
High quality sequence stop: 759.
Location/Qualifiers
1. .768
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_97"
/lab_host="DHI0B"
/notes="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site:1: BamHI; Site:2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
```


Query Match 100.0%; Score 225; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.5e-103;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCCTTCTGTGATCTTCAGCAAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
|||||
DB 1 TATTTCCTTCTGTGATCTTCAGCAAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
|||||
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
|||||
DB 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
|||||
QY 121 TCCTACGATGGCCCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTCTGATAATC 180
|||||
DB 121 TCCTACGATGGCCCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTCTGATAATC 180
|||||
QY 181 ATCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
|||||
DB 181 ATCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
|||||

RESULT 2

US-08-299-849B-18
; Sequence 18, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
; APPLICANT: De plaen, Etienne; Boon-Falleur, Thierry;
; APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
; APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,849B
; FILING DATE: 1-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5612201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: MAGE-6 gene
US-08-299-849B-18

Query Match 100.0%; Score 225; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.5e-103;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCCTTCTGTGATCTTCAGCAAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
|||||
DB 1 TATTTCCTTCTGTGATCTTCAGCAAAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
|||||
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
|||||
DB 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
|||||
QY 121 TCCTACGATGGCCCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTCTGATAATC 180
|||||
DB 121 TCCTACGATGGCCCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTCTGATAATC 180
|||||
QY 181 ATCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
|||||
DB 181 ATCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
|||||

RESULT 3

US-08-142-368A-18
; Sequence 18, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
; APPLICANT: Van den Eynde, Beno t; Van pel, Aline; De Plaen, Etienne;
; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,368A
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 592572man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5253.4-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: MAGE-6 gene
; US-08-142-368A-18

Query Match 100.0%; Score 225; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.5e-103;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
Db 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120

QY 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCCCTGATAATC 180
Db 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCCCTGATAATC 180

QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
Db 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225

RESULT 4
US-08-967-727-18
; Sequence 18, Application US/08967727
; Patent No. 6025474
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,727
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: MAGE-6 gene
; US-08-967-727-18

Query Match 100.0%; Score 225; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.5e-103;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
Db 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120

QY 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCCCTGATAATC 180
Db 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCCCTGATAATC 180

QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
Db 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225

RESULT 5
US-08-037-230D-18
; Sequence 18, Application US/08037230D
; Patent No. 6235525
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,727
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US/08/037,230D
FILING DATE: 26-MARCH-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6235525man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: MAGE-6 gene
US-08-037-230D-18

Query Match 100.0%; Score 225; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.5e-103;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCCGACCTGGTCTTTGGCATC 60
Db 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCCGACCTGGTCTTTGGCATC 60

Qy 61 GAGCTGATGGAAGTGGACCCATCGCCACGTGTACATCTTTGGCACCTGCTGGGCCTC 120
Db 61 GAGCTGATGGAAGTGGACCCATCGCCACGTGTACATCTTTGGCACCTGCTGGGCCTC 120

Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGTGCCAGACAGGCTTCTGATATC 180
Db 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGTGCCAGACAGGCTTCTGATATC 180

Qy 181 ATCCTGGCCATAATCGCAAGAGGGGACGTGTCCTCTGAGGAG 225
Db 181 ATCCTGGCCATAATCGCAAGAGGGGACGTGTCCTCTGAGGAG 225

RESULT 6
US-09-056-105-7
Sequence 7, Application US/09056105
Patent No. 6287569
GENERAL INFORMATION:
APPLICANT: KIPPS, THOMAS J.
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 945
TYPE: DNA
ORGANISM: Homo sapiens
US-09-056-105-7

Query Match 69.8%; Score 157; DB 4; Length 945;
Best Local Similarity 100.0%; Pred. No. 2.9e-69;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
Db 436 TTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 495

Qy 64 CTGATGGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 123
Db 496 CTGATGGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 123

Qy 124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCCA 160
Db 556 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCCA 592

RESULT 7
US-09-056-105-13
Sequence 13, Application US/09056105
Patent No. 6287569
GENERAL INFORMATION:
APPLICANT: KIPPS, THOMAS J.
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
EARLIER FILING DATE: 1998-04-06
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 1019
TYPE: DNA
ORGANISM: Homo sapiens
US-09-056-105-13

Query Match 69.8%; Score 157; DB 4; Length 1019;
Best Local Similarity 100.0%; Pred. No. 2.9e-69;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 63
Db 501 TTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATCGAG 560

Qy 64 CTGATGGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 123
Db 561 CTGATGGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCTCTCC 620

Qy 124 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCCA 160
Db 621 TACGATGGCCTGCTGGGTGACAATCAGATCATGCCCCA 657

RESULT 8
US-08-993-738A-2
Sequence 2, Application US/08993738A
Patent No. 5928938
GENERAL INFORMATION:
APPLICANT: van der Bruggen, Pierre; Deplaen Etienne;
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Peptides Which Complex With

;; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fulbright & Jaworski L.L.P.
;; STREET: 805 Third Avenue
;; CITY: New York City
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10022
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
;;
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/993,738A
;; FILING DATE: 19-December-1997
;; CLASSIFICATION: 536
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/713,354
;; FILING DATE: 13-September-1996
;; CLASSIFICATION: 536
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 5928938man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5460.1 DIV - JEL/NDH
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1375 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-08-993-738A-2

Query Match 69.8%; Score 157; DB 2; Length 1375;
Best Local Similarity 100.0%; Pred. No. 2.9e-69;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCCTTGACAGCTGGTCTTTGGCATCGAG 63
Db 595 TTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCCTTGACAGCTGGTCTTTGGCATCGAG 654

Qy 64 CTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 123
Db 655 CTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 714

Qy 124 TACGATGCGCTGCTGGGTGACAAATCAGATCATGCCCA 160
Db 715 TACGATGCGCTGCTGGGTGACAAATCAGATCATGCCCA 751

RESULT 9
US-08-713-354C-2
;; Sequence 2, Application US/08713354C
;; Patent No. 6265215
;; GENERAL INFORMATION:
;; APPLICANT: van der Bruggen, Pierre; DePlaen Etienne;
;; APPLICANT: Boon-Falleur, Thierry
;; TITLE OF INVENTION: Isolated Peptides Which Complex With
;; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Felfe & Lynch
;; STREET: 805 Third Avenue
;; CITY: New York City
;; STATE: New York
;; ZIP: 10022
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/713,354C
;; FILING DATE: 13-September-1996
;; CLASSIFICATION: 536
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 6265215man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5460
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1375 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;;
;; US-08-713-354C-2

Query Match 69.8%; Score 157; DB 4; Length 1375;
Best Local Similarity 100.0%; Pred. No. 2.9e-69;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCCTTGACAGCTGGTCTTTGGCATCGAG 63
Db 595 TTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCCTTGACAGCTGGTCTTTGGCATCGAG 654

Qy 64 CTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 123
Db 655 CTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCTGGGCTCTCC 714

Qy 124 TACGATGCGCTGCTGGGTGACAAATCAGATCATGCCCA 160
Db 715 TACGATGCGCTGCTGGGTGACAAATCAGATCATGCCCA 751

RESULT 10
US-07-807-043B-11
;; Sequence 11, Application US/07807043B
;; Patent No. 5342774
;; GENERAL INFORMATION:
;; APPLICANT: Boop, Thierry, Van den Eynde, Beno t
;; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
;; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Felfe & Lynch
;; STREET: 805 Third Avenue
;; CITY: New York City
;; STATE: New York
;; ZIP: 10022
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;;
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/807,043B
;; FILING DATE: 19911212
;; CLASSIFICATION: 424
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/764,364
;; FILING DATE: 23-SEPTEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/728,838
;; FILING DATE: 9-JULY-1991
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/705,702
;; FILING DATE: 23-May-1991

```
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hanson, No. 5342774man D.
;   REGISTRATION NUMBER: 30,946
;   REFERENCE/DOCKET NUMBER: LUD 253.3
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 688-9200
;   TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1640 base pairs
;     TYPE: NUCLEIC ACID
;     STRANDEDNESS: singular
;     TOPOLOGY: linear
;     MOLECULE TYPE: cdna to mRNA
;     FEATURE:
;       NAME/KEY: cdna MAGE-3
; US-07-807-043B-11
;
; Query Match 32.9%; Score 74; DB 1; Length 1640;
; Best Local Similarity 99.2%; Pred. No. 5.4e-28;
; Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 36 TTCCTTGCAGCTGCTCTTTGGCATCGAGCTGATGGAAGTGACCCCATCGGCCACGTGTA 95
;   |||||||
; Db 639 TTCCTTGCAGCTGCTCTTTGGCATCGAGCTGATGGAAGTGACCCCATCGGCCACGTGTA 698
;
; QY 96 CATCTTTGCCACCTGCGCTGGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
;   |||||||
; Db 699 CATCTTTGCCACCTGCGCTGGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 758
;
; QY 156 GCCCA 160
;   |||||
; Db 759 GCCCA 763
;
; RESULT 11
; US-08-299-849B-11
; Sequence 11, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
;   APPLICANT: De plaen, Etienne; Boon-Falleur, Thierry;
;   APPLICANT: Leth, Bernard; Szkora, Jean-Pierre; De Smet, Charles;
;   APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Felfe & Lynch
;   STREET: 805 Third Avenue
;   CITY: New York City
;   STATE: New York
;   ZIP: 10022
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;   COMPUTER: IBM
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/299,849B
;   FILING DATE: 1-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/037,230
;   FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US92/04354
;   FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/807,043
;   FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/764,364
```

```
;
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/728,838
;   APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/705,702
;   FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Hanson, No. 5612201man D.
;   REGISTRATION NUMBER: 30,946
;   REFERENCE/DOCKET NUMBER: LUD 5355
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) 688-9200
;   TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1640 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: cdna to mRNA
;     FEATURE:
;       NAME/KEY: cdna MAGE-3
; US-08-299-849B-11
;
; Query Match 32.9%; Score 74; DB 1; Length 1640;
; Best Local Similarity 99.2%; Pred. No. 5.4e-28;
; Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 36 TTCCTTGCAGCTGCTCTTTGGCATCGAGCTGATGGAAGTGACCCCATCGGCCACGTGTA 95
;   |||||||
; Db 639 TTCCTTGCAGCTGCTCTTTGGCATCGAGCTGATGGAAGTGACCCCATCGGCCACGTGTA 698
;
; QY 96 CATCTTTGCCACCTGCGCTGGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
;   |||||||
; Db 699 CATCTTTGCCACCTGCGCTGGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 758
;
; QY 156 GCCCA 160
;   |||||
; Db 759 GCCCA 763
;
; RESULT 12
; US-08-142-368A-11
; Sequence 11, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
;   APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
;   APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
;   APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Felfe & Lynch
;   STREET: 805 Third Avenue
;   CITY: New York City
;   STATE: New York
;   ZIP: 10022
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;   COMPUTER: IBM
;   OPERATING SYSTEM: PC-DOS
;   SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/142,368A
;   FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US92/04354
;   FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
```


APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 592572man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: cDNA MAGE-3
US-08-142-368A-11

Query Match 32.9%; Score 74; DB 2; Length 1640;
Best Local Similarity 99.2%; Pred. No. 5.4e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGTGTA 95
Db 639 TTTCTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGTGTA 698
QY 96 CATCTTTGCCACCTGCTCTTGGCGCTCTCTCTACGATGGCGCTGCTGGTGACAAATCAGATCAT 155
Db 699 CATCTTTGCCACCTGCTCTTGGCGCTCTCTCTACGATGGCGCTGCTGGTGACAAATCAGATCAT 758
QY 156 GCCCA 160
Db 759 GCCCA 763

RESULT 13
US-08-967-727-11
Sequence 11, Application US/08967727
Patent No. 6025474
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: Wordperfect
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,727
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 602547man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: cDNA MAGE-3
US-08-967-727-11

Query Match 32.9%; Score 74; DB 3; Length 1640;
Best Local Similarity 99.2%; Pred. No. 5.4e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TTCTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGTGTA 95
Db 639 TTTCTTCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGTGTA 698
QY 96 CATCTTTGCCACCTGCTCTTGGCGCTCTCTCTACGATGGCGCTGCTGGTGACAAATCAGATCAT 155
Db 699 CATCTTTGCCACCTGCTCTTGGCGCTCTCTCTACGATGGCGCTGCTGGTGACAAATCAGATCAT 758
QY 156 GCCCA 160
Db 759 GCCCA 763

RESULT 14
US-08-037-230d-11
Sequence 11, Application US/08037230D
Patent No. 6235525
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/037, 230D
;; FILING DATE: 26-MARCH-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/04354
;; FILING DATE: 22-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/807,043
;; FILING DATE: 12-DECEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/764,364
;; FILING DATE: 23-SEPTEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/728,838
;; FILING DATE: 9-JULY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/705,702
;; FILING DATE: 23-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 6235525man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5353
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1640 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA to mRNA
;; FEATURE:
;; NAME/KEY: CDNA MAGE-3
US-08-037-230D-11

Query Match 32.9%; Score 74; DB 4; Length 1640;
Best Local Similarity 99.2%; Pred. No. 5.4e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
|||||
Db 639 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 698
|||||
Qy 96 CATCTTTGCCACCTGCCTGGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 699 CATCTTTGCCACCTGCCTGGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 758
|||||
Qy 156 GCCCA 160
|||||
Db 759 GCCCA 763

RESULT 15
US-08-928-615-1
; Sequence 1, Application US/08928615
; Patent No. 5965535
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.

;; ZIP: 02210-2211
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/928,615
;; FILING DATE:
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Van Amsterdam, John R.
;; REGISTRATION NUMBER: 40,212
;; REFERENCE/DOCKET NUMBER: L0461/7017
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-720-3500
;; TELEFAX: 617-720-2441
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 4204 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FEATURE:
;; NAME/KEY: Coding Sequence
;; LOCATION: 2465...3406
US-08-928-615-1

Query Match 32.9%; Score 74; DB 2; Length 4204;
Best Local Similarity 99.2%; Pred. No. 5.3e-28;
Matches 124; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 36 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 95
|||||
Db 2932 TTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTA 2991
|||||
Qy 96 CATCTTTGCCACCTGCCTGGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 155
|||||
Db 2992 CATCTTTGCCACCTGCCTGGGCCCTCTCTACGATGGCTGCTGGTGACAAATCAGATCAT 3051
|||||
Qy 156 GCCCA 160
|||||
Db 3052 GCCCA 3056

Search completed: May 9, 2002, 23:45:11
Job time: 7788 sec

THIS PAGE BLANK (USPTO)